

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 16:40:19 ; Search time 6893 Seconds  
(without alignments)  
11343.513 Million cell updates/sec

Title: US-09-668-314C-1  
Perfect score: 1804  
Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
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23: em\_pat:\*  
24: em\_ph:\*  
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26: em\_ro:\*  
27: em\_sts:\*

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28: em_un:*
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33: em_htg_mus:*
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39: em_htgo_hum:*
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41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1804	100.0	1804	6	BD235885	BD235885 Alzheimer
2	1804	100.0	1804	6	AR224092	AR224092 Sequence
3	1804	100.0	1804	6	AR269223	AR269223 Sequence
4	1804	100.0	1804	6	AX105383	AX105383 Sequence
5	1804	100.0	1804	6	AX573821	AX573821 Sequence
6	1804	100.0	1804	9	AF200342	AF200342 Homo sapi
7	1790.6	99.3	2990	9	AF178532	AF178532 Homo sapi
8	1788.2	99.1	1885	9	AF200192	AF200192 Homo sapi
9	1784.4	98.9	1879	6	AX376004	AX376004 Sequence
10	1784.4	98.9	1879	9	AY358927	AY358927 Homo sapi
11	1768.2	98.0	1864	9	BC014453	BC014453 Homo sapi
12	1768.2	98.0	1873	6	BD231786	BD231786 Metastati
13	1768.2	98.0	1873	6	AR411231	AR411231 Sequence
14	1768.2	98.0	1873	9	AF117892	AF117892 Homo sapi
15	1765.6	97.9	1862	6	AR136909	AR136909 Sequence
16	1765.6	97.9	1862	6	E30679	E30679 ASP1. 6/200
17	1765.6	97.9	1862	6	AX775211	AX775211 Sequence
18	1765.6	97.9	1862	6	BD165905	BD165905 ASP1. 1/2
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20	1753.4	97.2	1863	6	AX351516	AX351516 Sequence
21	1753.4	97.2	1863	9	AF050171	AF050171 Homo sapi
22	1550	85.9	1621	9	AF212252	AF212252 Homo sapi
23	1483.6	82.2	1712	6	AX136403	AX136403 Sequence
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25	1483.6	82.2	1712	9	AK075539	AK075539 Homo sapi
26	1482.2	82.2	2840	9	AF188276	AF188276 Homo sapi
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28	1478.6	82.0	2429	6	AR411214	AR411214 Sequence
29	1442.6	80.0	2821	9	AF188277	AF188277 Homo sapi
30	1263.2	70.0	1494	6	AX879009	AX879009 Sequence
31	1263.2	70.0	1494	6	BD157592	BD157592 Primer fo
32	1263.2	70.0	1494	9	AK027376	AK027376 Homo sapi
33	1179.4	65.4	1774	10	AF216310	AF216310 Mus muscu

34	1134.2	62.9	1545	6	AR170159	AR170159 Sequence
35	1134.2	62.9	1545	6	AR201145	AR201145 Sequence
36	1104.6	61.2	2514	6	AR263854	AR263854 Sequence
37	953.6	52.9	1021	6	AR263907	AR263907 Sequence
38	634.6	35.2	3516	5	BC059963	BC059963 Xenopus l
39	625.2	34.7	2568	5	BC055989	BC055989 Xenopus l
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41	568.6	31.5	845	6	AX866692	AX866692 Sequence
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c 43	496	27.5	554	6	AX136731	AX136731 Sequence
c 44	496	27.5	554	6	BD123971	BD123971 Secretory
45	494	27.4	45566	9	HS44C5	AL773570 Homo sapi

# ALIGNMENTS

RESULT 1  
BD235885  
LOCUS BD235885 1804 bp DNA linear PAT 17-JUL-2003  
DEFINITION Alzheimer's disease secretase.  
ACCESSION BD235885  
VERSION BD235885.1 GI:33045655  
KEYWORDS JP 2002526081-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1804)  
AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and  
Yan,R.  
TITLE Alzheimer's disease secretase  
JOURNAL Patent: JP 2002526081-A 1 20-AUG-2002;  
PHARMACIA AND UPJOHN CO  
COMMENT OS Homo sapiens (human)  
PN JP 2002526081-A/1  
PD 20-AUG-2002  
PF 23-SEP-1999 JP 2000574268  
PR 24-SEP-1998 US 60/101594  
PI MARK E GURNEY,MICHAEL JEROME BIENKOWSKI,ROBERT LEROY PI  
HEINRIKSON,  
PI LUIS A PARODI,RIQIANG YAN  
PC C12N15/09,A61K45/00,A61P25/28,C07K14/47,C07K16/18,C12N1/15, PC  
C12N1/19,  
PC  
C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12P21/08,C12Q1/37,G01N33/ PC  
15,  
PC G01N33/50//(C12N1/21,C12R1:19),C12N15/00,C12N5/00 CC  
Alzheimer's disease secretase  
FH Key Location/Qualifiers  
FT source 1. .1804  
FT /organism='Homo sapiens (human)'.  
FEATURES Location/Qualifiers  
source 1. .1804  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match		100.0%;	Score 1804;	DB 6;	Length 1804;	
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Matches 1804;		Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Qy	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCCAGTGGCTCCTGCGCGCC	60			
Db	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCCAGTGGCTCCTGCGCGCC	60			
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	120			
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	120			
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180			
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180			
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG	240			
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG	240			
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300			
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300			
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTGCCGTGGCAGGA	360			
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTGCCGTGGCAGGA	360			
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420			
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420			
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480			
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480			
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540			
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540			
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600			
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600			
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660			
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660			
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720			
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720			
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAAA	780			
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAAA	780			



Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
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Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620



Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
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Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
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Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
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Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
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Qy	1021	CAGCTGGCGTGCTGGACGAATTTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
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Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
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Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
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Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 3  
AR269223  
LOCUS

AR269223

1804 bp

DNA

linear

PAT 10-APR-2003

DEFINITION Sequence 1 from patent US 6500667.  
 ACCESSION AR269223  
 VERSION AR269223.1 GI:29700191  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 1804)  
 AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and Yan,R.  
 TITLE Aspartyl protease 2 (Asp2) antisense oligonucleotides  
 JOURNAL Patent: US 6500667-A 1 31-DEC-2002;  
 FEATURES Location/Qualifiers  
     source 1. .1804  
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ORIGIN

Query Match 100.0%; Score 1804; DB 6; Length 1804;  
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 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
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Qy	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
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Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
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Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
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Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
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Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
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Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTGCGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTGCGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380

Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

#### RESULT 4

AX105383

LOCUS AX105383 1804 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 1 from Patent WO0123533.

ACCESSION AX105383

VERSION AX105383.1 GI:13921510

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gurney,M. and Bienkowski,M.J.

TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor

JOURNAL Patent: WO 0123533-A 1 05-APR-2001;  
Pharmacia & Upjohn Company (US)

FEATURES Location/Qualifiers

source 1. .1804  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

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Query Match 100.0%; Score 1804; DB 6; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC 300
      |||
Db    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
      |||
Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy    361 ACCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db    361 ACCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

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      |||
Db    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT 540
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Db    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

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Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy    781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCGTGTCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCGTGTCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTACAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTACAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
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Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
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Qy      1801 AAAA 1804
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Db      1801 AAAA 1804

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# RESULT 5

AX573821

LOCUS AX573821 1804 bp DNA linear PAT 07-JAN-2003

DEFINITION Sequence 1 from Patent EP1249498.

ACCESSION AX573821

VERSION AX573821.1 GI:27551476

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gurney,M. and Bienkowski,M.J.

TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor

JOURNAL Patent: EP 1249498-A 1 16-OCT-2002;

PHARMACIA & UPJOHN COMPANY (US)

FEATURES

source

Location/Qualifiers

1. .1804

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1804; DB 6; Length 1804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAAGTGGCTCCTGCGCGCC 60
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Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAAGTGGCTCCTGCGCGCC 60
Qy      61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db      61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 120
Qy      121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db      121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG 240
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Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
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Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
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Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
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Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
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Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
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Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
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Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
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Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
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Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
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Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
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Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
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Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 6  
AF200342  
LOCUS

AF200342

1804 bp

mRNA

linear

PRI 12-DEC-1999

DEFINITION Homo sapiens chromosome 21 aspartyl protease 1 mRNA, complete cds.  
 ACCESSION AF200342  
 VERSION AF200342.1 GI:6561811  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1804)  
 AUTHORS Yan,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,  
 Pauley,A.M., Brashier,J.R., Stratman,N.C., Mathews,W.R., Buhl,A.E.,  
 Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and  
 Gurney,M.E.  
 TITLE Membrane-anchored aspartyl protease with Alzheimer's disease  
 beta-secretase activity  
 JOURNAL Nature 402 (6761), 533-537 (1999)  
 MEDLINE 20057170  
 PUBMED 10591213  
 REFERENCE 2 (bases 1 to 1804)  
 AUTHORS Bienkowski,M.J., Shuck,M.E., Slightom,J.L. and Drong,R.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjohn, 301  
 Henrietta, Kalamazoo, MI 49007, USA  
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# ORIGIN

Query Match 100.0%; Score 1804; DB 9; Length 1804;  
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 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	GCCCCGAGCTGGCCCCCGCGCCCTTACGCTGCCCCCTCCGGGTGGCCGCGCCACGAAC	120
Db	61	GCCCCGAGCTGGCCCCCGCGCCCTTACGCTGCCCCCTCCGGGTGGCCGCGCCACGAAC	120

Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCCAACTTCTTGCCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCCAACTTCTTGCCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
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Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
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Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
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Db	601	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960

Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTAGCCCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Db	1141	ATTAGCCCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAAGAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAAGAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
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Qy	1801	AAAA	1804

Db 1801 AAAA 1804

RESULT 7  
AF178532  
LOCUS AF178532 2990 bp mRNA linear PRI 21-SEP-2000  
DEFINITION Homo sapiens aspartyl protease (BACE2) mRNA, complete cds.  
ACCESSION AF178532  
VERSION AF178532.1 GI:6851265  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2990)  
AUTHORS Solans,A., Estivill,X. and de La Luna,S.  
TITLE A new aspartyl protease on 21q22.3, BACE2, is highly similar to  
Alzheimer's amyloid precursor protein beta-secretase  
JOURNAL Cytogenet. Cell Genet. 89 (3-4), 177-184 (2000)  
MEDLINE 20422477  
PUBMED 10965118  
REFERENCE 2 (bases 1 to 2990)  
AUTHORS Solans,A., Estivill,X. and de la Luna,S.  
TITLE Direct Submission  
JOURNAL Submitted (18-AUG-1999) Medical and Molecular Genetics Center, IRO,  
Avia. Castelldefels Km 2,7, L'Hospitalet de Llobregat, Barcelona  
08907, Spain  
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/gene="BACE2"

ORIGIN

Query Match 99.3%; Score 1790.6; DB 9; Length 2990;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1793; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db	1184	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	1243
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Db	1244	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	1303
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	1304	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1363
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1364	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1423
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1424	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1483
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1484	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1543
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1544	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1603
Qy	1141	ATTAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
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Db	1664	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1723
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1724	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1783
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1784	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1843
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1844	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1903
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1904	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1963
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1964	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	2023
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
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 Db 2144 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 2203  
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 Db 2204 CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAACTTCATTCTAAACCAAAACAGA 2260

# RESULT 8

AF200192

LOCUS AF200192 1885 bp mRNA linear PRI 16-FEB-2000

DEFINITION Homo sapiens memapsin 1 mRNA, complete cds.

ACCESSION AF200192

VERSION AF200192.1 GI:6470290

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1885)

AUTHORS Lin,X., Koelsch,G., Wu,S., Downs,D., Dashti,A. and Tang,J.

TITLE Human aspartic protease memapsin 2 cleaves the beta-secretase site of beta-amyloid precursor protein

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1456-1460 (2000)

MEDLINE 20144060

PUBMED 10677483

REFERENCE 2 (bases 1 to 1885)

AUTHORS Lin,X., Koelsch,G. and Tang,J.

TITLE Direct Submission

JOURNAL Submitted (28-OCT-1999) Protein Studies Program, Oklahoma Medical Research Foundation, 825 N.E. 13th Street, Oklahoma City, OK 73104, USA

## FEATURES

source

Location/Qualifiers

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CDS

78..1634

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ORIGIN

Query Match 99.1%; Score 1788.2; DB 9; Length 1885;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1801; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db	138	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGACCGCGGCCACGAAC	197
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	198	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	257
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
Db	258	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	317
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
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Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
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Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
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Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT	540
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Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
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Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
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Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
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Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1158	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1217
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
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Db	1338	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1397
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1398	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1457
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
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Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
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 Db 1878 AAAAA 1882

# RESULT 9

AX376004

LOCUS AX376004 1879 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 71 from Patent WO0168848.

ACCESSION AX376004

VERSION AX376004.1 GI:19170395

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,  
 Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and  
 Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same

JOURNAL Patent: WO 0168848-A 71 20-SEP-2001;  
 Genentech, Inc. (US)

FEATURES Location/Qualifiers  
 source 1. .1879  
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## ORIGIN

Query Match 98.9%; Score 1784.4; DB 6; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153  
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Db	154	GCCCCGGAGCTGGCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	213
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Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
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Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
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 ACCESSION AY358927  
 VERSION AY358927.1 GI:37182971  
 KEYWORDS FLI\_CDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1879)  
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
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 Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wieand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.  
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
 PUBMED 12975309  
 REFERENCE 2 (bases 1 to 1879)  
 AUTHORS Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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ORIGIN

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
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Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
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Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
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RESULT 11

BC014453

LOCUS BC014453 1864 bp mRNA linear PRI 04-OCT-2003

DEFINITION Homo sapiens beta-site APP-cleaving enzyme 2, transcript variant a, mRNA (cDNA clone MGC:23029 IMAGE:4868925), complete cds.

ACCESSION BC014453

VERSION BC014453.1 GI:15680203

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1864)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1864)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

## COMMENT

Contact: MGC help desk  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcgsc.bc.ca  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline  
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 34 Row: 1 Column: 22  
This clone was selected for full length sequencing because it  
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## FEATURES

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Query Match 98.0%; Score 1768.2; DB 9; Length 1864;  
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Db	272	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGCGCCGCCAACTTCTTGCCCATG	331
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Db	332	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC	391
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	392	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	451
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	452	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	511
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGGCTTCGTTGGGGAA	480
Db	512	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGGCTTCGTTGGGGAA	571
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	572	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	631
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	632	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	691
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	692	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	751

Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	752	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	811
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	812	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	871
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	872	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	931
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	932	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	991
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	992	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1051
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1052	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1111
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1112	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1171
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1172	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1231
Qy	1141	ATTTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1232	ATTTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1291
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1292	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1351
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1352	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1411
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1412	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1471
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1472	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1531
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1532	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1591
Qy	1501	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560

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Db      1592 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1651
Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db      1652 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1711
Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
      |||
Db      1712 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1771
Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
      |||
Db      1772 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1831
Qy      1741 CTCCTACTTCCAAGAAAAATAATTAAAAAAA 1773
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Db      1832 CTCCTACTTCCAAGAAAAAAAAAAAAAAAAAAAA 1864

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# RESULT 12

BD231786

LOCUS BD231786 1873 bp DNA linear PAT 17-JUL-2003

DEFINITION Metastatic breast and colon cancer regulated genes.

ACCESSION BD231786

VERSION BD231786.1 GI:33041556

KEYWORDS JP 2002513542-A/18.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Xin,H. and Giese,K.

TITLE Metastatic breast and colon cancer regulated genes

JOURNAL Patent: JP 2002513542-A 18 14-MAY-2002;

CHIRON CORP

COMMENT OS Homo sapiens (human)

PN JP 2002513542-A/18

PD 14-MAY-2002

PF 24-DEC-1998 JP 2000526659

PR 31-DEC-1997 US 60/070112

PI HONG XIN,KLAUSE GIESE

PC C12N15/00,C07K14/47,C07K16/18,C07K19/00,C12N9/64,C12N15/09, PC  
C12Q1/68,

PC G01N33/50//A61K45/00,A61P35/04,C12N15/00,C12N15/00 CC

Metastatic breast and colon cancer regulated genes FH Key

Location/Qualifiers

FT source 1. .1873

FT /organism='Homo sapiens (human)'. Location/Qualifiers

FEATURES 1. .1873

source /organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

Query Match 98.0%; Score 1768.2; DB 6; Length 1873;



Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db     101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160
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Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
      |||
Db     161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 220
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Qy     121 CGCGTAGTTGCGCCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
      |||
Db     221 CGCGTAGTTGCGCCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280
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Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG 240
      |||
Db     281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG 340
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Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC 300
      |||
Db     341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC 400
      |||

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
      |||
Db     401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460
      |||

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
      |||
Db     461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 520
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Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
      |||
Db     521 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580
      |||

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
      |||
Db     581 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 640
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Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
      |||
Db     641 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 700
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Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
      |||
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      |||

Qy     661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
      |||
Db     761 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 820
      |||

Qy     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db     821 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 880
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Qy     781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db	881	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAATTCTGAAA	940
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	941	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1000
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1001	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1060
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1061	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1120
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1121	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1180
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1181	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1240
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCA	1200
Db	1241	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCA	1300
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1301	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1360
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1361	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1420
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1421	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1480
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1481	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1540
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTACAGCGTCGCCCC	1500
Db	1541	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTACAGCGTCGCCCC	1600
Qy	1501	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1601	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1660
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1661	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1720
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1721	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1780

QY 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
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 Db 1781 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840  
 QY 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1773  
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 Db 1841 CTCCCTACTTCCAAGAAAAAAA 1873

RESULT 13

AR411231

LOCUS AR411231 1873 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 18 from patent US 6635748.

ACCESSION AR411231

VERSION AR411231.1 GI:40163285

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Xin,H. and Giese,K.

TITLE Metastatic breast and colon cancer regulated genes

JOURNAL Patent: US 6635748-A 18 21-OCT-2003;

FEATURES Location/Qualifiers

source 1..1873

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 98.0%; Score 1768.2; DB 6; Length 1873;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60  
 |||  
 Db 101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160  
 QY 61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
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 Db 161 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 220  
 QY 121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
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 Db 221 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280  
 QY 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCAACTTCTTGGCCATG 240  
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 Db 281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCAACTTCTTGGCCATG 340  
 QY 241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300  
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 Db 341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400  
 QY 301 CCCCCGAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360  
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 Db 401 CCCCCGAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	461	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	520
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	521	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	580
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	581	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	640
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	641	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	700
Qy	601	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	701	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	760
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCTTGCT	720
Db	761	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCTTGCT	820
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	821	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	880
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTTCTGAAA	840
Db	881	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTTCTGAAA	940
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	941	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1000
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1001	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1060
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1061	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1120
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1121	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1180
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1181	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1240
Qy	1141	ATTGAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1241	ATTGAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1300

Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1301	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1360
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1361	AGAGCCCAGAAGAGGGTGGGCTTCGAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1420
Qy	1321	GTGTCTGAAATTTCCGGGCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1421	GTGTCTGAAATTTCCGGGCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1480
Qy	1381	CAGTCTTTGAGCGAGCCCATTGTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
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Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1541	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1600
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1601	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1660
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Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1680
Db	1721	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1780
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Db	1781	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1840
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAA	1773
Db	1841	CTCCCTACTTCCAAGAAAAAAA	1873

# RESULT 14

AF117892

LOCUS AF117892 1873 bp mRNA linear PRI 14-JUL-2000

DEFINITION Homo sapiens aspartic-like protease mRNA, complete cds.

ACCESSION AF117892

VERSION AF117892.1 GI:5565865

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Xin,H., Stephans,J.C., Duan,X., Harrowe,G., Kim,E., Grieshammer,U., Kingsley,C. and Giese,K.

TITLE Identification of a novel aspartic-like protease differentially expressed in human breast cancer cell lines

JOURNAL Biochim. Biophys. Acta 1501 (2-3), 125-137 (2000)  
 MEDLINE 20298348  
 PUBMED 10838186  
 REFERENCE 2 (bases 1 to 1873)  
 AUTHORS Xin,H., Stephans,J.C., Duan,X., Harrowe,G., Kim,E., Grieshammer,U.  
 and Glese,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-JAN-1999) Technologies, Chiron Co., 4560 Horton St.,  
 4.5103, Emeryville, CA 94608, USA  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
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 EDVASNCVPAQSLSEPI LWIVSYALMSVCGAILLV LIVLLLLLPFRQRRPRDPEVND  
 ESSLVRHRWK"

# ORIGIN

Query Match 98.0%; Score 1768.2; DB 9; Length 1873;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC	60
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Db	161	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	220
Qy	121	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	221	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	280
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG	240
Db	281	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG	340
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
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Db	641	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	700
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
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Db	761	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCTTGCT	820
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Db	821	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	880
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Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1181	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1240
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RESULT 15

AR136909

LOCUS AR136909 1862 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 1 from patent US 6162630.

ACCESSION AR136909

VERSION AR136909.1 GI:14478159

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1862)

AUTHORS Powell,D.J., Southan,C., Chapman,C.G. and Evans,J.R.

TITLE ASP1



JOURNAL Patent: US 6162630-A 1 19-DEC-2000;  
FEATURES Location/Qualifiers  
source 1. .1862  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN

Query Match 97.9%; Score 1765.6; DB 6; Length 1862;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1768; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db      91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 150

QY      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
      |||
Db     151 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 210

QY     121 CGCGTAGTTGCGCCCAACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
      |||
Db     211 CGCGTAGTTGCGCCCAACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 270

QY     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCGCAACTTCTTGCCCATG 240
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QY     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
      |||
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QY     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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QY     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
      |||
Db     511 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 570

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 QY 1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTACAGCGTCGCCCC 1500  
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 Job time : 6904 secs

OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 16:24:13 ; Search time 701 Seconds  
(without alignments)  
10932.595 Million cell updates/sec

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Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

## RESULT 1

AAA15661

ID AAA15661 standard; cDNA; 1804 BP.

XX

AC AAA15661;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human aspartyl protease 1 (Asp1) nucleotide sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;

KW Alzheimer's disease; beta secretase site; ss.

XX

OS Homo sapiens.

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XX      WO200017369-A2.
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XX      30-MAR-2000.
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XX      23-SEP-1999;    99WO-US020881.
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XX      24-SEP-1998;    98US-0101594P.
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XX      (PHAA ) PHARMACIA & UPJOHN CO.
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XX      Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
XX      WPI; 2000-303209/26.
XX      P-PSDB; AAY88424.
XX
XX      New enzyme designated human aspartase useful in research into Alzheimer's
XX      Disease is capable of cleaving amyloid protein precursor at the beta
XX      secretase site to produce amyloid beta peptide.
XX
XX      Claim 11; Fig 1; 183pp; English.
XX
XX      This sequence represents the human aspartyl protease nucleotide sequence.
XX      The invention relates to a protease capable of cleaving the beta
XX      secretase site of amyloid precursor protein (APP). The protease contains
XX      a sequence encoding the amino acid sequence DTG and a sequence encoding
XX      DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
XX      causes an autosomal dominant form of Alzheimer's disease. APP localises
XX      to the cell surface membrane and have a single C-terminal transmembrane
XX      domain. Proteolytic processing of APP produces the amyloid beta protein,
XX      which is possibly very important in Alzheimer's disease. The invention
XX      includes a nucleotide sequence encoding the protease, a vector containing
XX      the nucleotide sequence, and a cell line comprising the vector. Methods
XX      for screening for inhibitors of beta secretase activity are also given in
XX      the invention. The human aspartase protein and nucleotide sequences and
XX      the methods for identifying inhibitors of the protease, are useful in the
XX      treatment of and research in to Alzheimer's disease
XX
XX      Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;
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XX
XX      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGGCGCCGCAACTTCTTGGCCATG 240

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Qy	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781		GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781		GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021		CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTGAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Db	1141	ATTGAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 2  
AAS11701



ID AAS11701 standard; DNA; 1804 BP.  
XX  
AC AAS11701;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE DNA encoding human aspartyl protease 1 (Asp-1).  
XX  
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;  
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;  
KW beta-secretase; Alzheimer's disease; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1. .1557  
FT /\*tag= a  
FT /product= "Aspartyl protease-1 (Asp-1)"  
XX  
PN WO200149097-A2.  
XX  
PD 12-JUL-2001.  
XX  
PF 09-MAY-2001; 2001WO-IB000797.  
XX  
PR 09-MAY-2001; 2001WO-IB000797.  
XX  
PA (BIEN/) BIENKOWSKI M J.  
PA (GURN/) GURNEY M E.  
PA (HEIN/) HEINRIKSON R L.  
PA (PARO/) PARODI L A.  
PA (YANR/) YAN R.  
XX  
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
XX  
DR WPI; 2001-502548/55.  
DR P-PSDB; AAU07201.  
XX  
PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity.  
XX  
PS Example 2; Fig 1; 185pp; English.  
XX  
CC The invention relates to a novel purified polypeptide comprising a  
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the  
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide  
CC and the fragment retain the beta-secretase activity of the mammalian Asp2  
CC protein. Also included is an isoform of amyloid protein precursor (APP)  
CC comprising the amino acid sequence of a APP or its fragment containing an  
CC APP cleavage site recognisable by a mammalian beta-secretase, and further  
CC comprising two lysine residues at the carboxyl terminus of the amino acid  
CC sequence of the mammalian APP or APP fragment. The polypeptides are used  
CC for assaying for modulators of beta-secretase activity; identifying  
CC agents that inhibit the APP processing activity of human Asp2 aspartyl  
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2

CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.  
CC Agents identified by the above methods are useful for treating  
CC Alzheimer's disease; and for identifying modulators of amyloid-beta  
CC (Abeta) peptide production, for use in designing therapeutics for the  
CC treatment or prevention of Alzheimer's disease. Probes and primers  
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp  
CC nucleic acids in in vitro assays and in Northern and Southern blots. The  
CC present sequence represents the coding sequence of human Asp-1  
XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660

Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCGGCCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCGGCCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500

QY	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
QY	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
QY	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
QY	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
QY	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
QY	1801	AAAA	1804
Db	1801	AAAA	1804

# RESULT 3

AAD17864

ID AAD17864 standard; cDNA; 1804 BP.

XX

AC AAD17864;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human aspartyl protease 1 (hu-Aspl) cDNA.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;

KW chromosome 21; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	CDS	1. .1557
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FT		/*tag= a
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FT		/product= "Human aspartyl protease 1"
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FT	sig_peptide	1. .60
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FT		/*tag= b
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FT	mat_peptide	61. .1554
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FT		/*tag= c
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FT		/product= "Mature human aspartyl protease 1"
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XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.  
 XX  
 PR 23-SEP-1999; 99US-00404133.  
 PR 23-SEP-1999; 99US-0155493P.  
 PR 23-SEP-1999; 99WO-US020881.  
 PR 13-OCT-1999; 99US-00416901.  
 PR 06-DEC-1999; 99US-0169232P.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Bienkowski MJ, Gurney M;  
 XX  
 DR WPI; 2001-444208/48.  
 DR P-PSDB; AAE10628.  
 XX  
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid  
 PT precursor protein processing activity and alpha-secretase activity, for  
 PT identifying modulators useful in treating Alzheimer's disease.  
 XX  
 PS Claim 30; Fig 1; 187pp; English.  
 XX  
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1  
 CC proteins which lack transmembrane domain or amino terminal domain or  
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid  
 CC protein precursor (APP) processing activity. The proteins of the  
 CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which  
 CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase  
 CC activity, where modulators that increase hu-Asp1 alpha-secretase  
 CC are useful for treating Alzheimer's disease (AD) which causes progressive  
 CC dementia with consequent formation of amyloid plaques, neurofibrillary  
 CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful  
 CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein  
 CC with the substrate under acidic conditions and determining the level of  
 CC hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding  
 CC human Asp1 protein. Asp1 gene is localised on chromosome 21  
 XX  
 SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;  
  
 Query Match 100.0%; Score 1804; DB 4; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 60  
 Db 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 60  
  
 Qy 61 GCGGCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
 Db 61 GCGGCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
  
 Qy 121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
 Db 121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
  
 Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG 240  
 Db 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG 240

Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACCTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACCTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 4

AAD13020

ID AAD13020 standard; cDNA; 1804 BP.

XX

AC AAD13020;  
 XX  
 DT 23-OCT-2001 (first entry)  
 XX  
 DE Human aspartyl protease 1 (Hu-Asp1) cDNA.  
 XX  
 KW Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;  
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;  
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;  
 KW neuroprotective; antisense therapy; gene therapy; chromosome 21; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .1557  
 FT /\*tag= a  
 FT /product= "Human aspartyl protease 1 (Hu-Asp1)"  
 FT sig\_peptide 1. .60  
 FT /\*tag= b  
 FT mat\_peptide 61. .1554  
 FT /\*tag= c  
 FT /product= "Mature human aspartyl protease 1 (Hu-Asp1)"  
 XX  
 PN WO200150829-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000799.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000799.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-483072/52.  
 DR P-PSDB; AAE06858.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 2; Fig 1; 185pp; English.  
 XX  
 CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid  
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.  
 CC Human aspartyl proteases can act as beta-secretase proteases useful for  
 CC treating Alzheimer's disease. APP isoforms are useful for identifying  
 CC modulators of amyloid-beta peptide production, for use in designing  
 CC therapeutics for the treatment and prevention of Alzheimer's disease,  
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis  
 CC and neuronal loss. APP isoforms are also used in methods for identifying



CC inhibitors and modulators of human Asp2 activity. The invention relates  
CC to a method for identifying agents that modulate the activity of human  
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used  
CC as a means to screen in cellular assays for the inhibitors of beta- and  
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in  
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-  
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.  
CC The present cDNA sequence encodes human aspartyl protease 1 (Hu-Asp1). Hu  
CC -Asp 1 gene is localised on chromosome 21  
XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
QY	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
QY	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
QY	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
QY	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
QY	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
QY	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
QY	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
QY	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT	540
QY	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
QY	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660

Db	601	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500

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Db      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
        |||||
Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
        |||||
Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTTCAATCTCTGTTCT 1680
        |||||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTTCAATCTCTGTTCT 1680
Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
        |||||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800
        |||||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800
Qy      1801 AAAA 1804
        ||||
Db      1801 AAAA 1804

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# RESULT 5

AAD06738

ID AAD06738 standard; cDNA; 1804 BP.

XX

AC AAD06738;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human aspartyl protease 1 (Asp 1) cDNA.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;  
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;  
 KW beta-secretase; chromosome 21; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1557

FT /\*tag= a

FT /product= "Human aspartyl protease 1 (Asp 1)"

FT sig\_peptide 1. .60

FT /\*tag= b

FT sig\_peptide 64. .186

FT /\*tag= c

FT /note= "Pre-pro-peptide"

FT sig\_peptide 67. .186

FT /\*tag= d

FT /note= "Pro-peptide"

FT mat\_peptide 187. .1554

FT /\*tag= e

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FT          /product= "Human mature aspartyl protease 1 (Asp 1)"
XX
PN      WO200123533-A2.
XX
PD      05-APR-2001.
XX
PF      22-SEP-2000; 2000WO-US026080.
XX
PR      23-SEP-1999; 99US-0155493P.
PR      23-SEP-1999; 99WO-US020881.
PR      13-OCT-1999; 99US-00416901.
PR      06-DEC-1999; 99US-0169232P.
XX
PA      (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI      Gurney M, Bienkowski MJ;
XX
DR      WPI; 2001-290516/30.
DR      P-PSDB; AAE02580.
XX
PT      Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT      protein, useful for the treatment of Alzheimer's disease.
XX
PS      Example 2; Fig 1; 189pp; English.
XX
CC      The present invention relates to enzymes for cleaving the alpha-
CC      secretase site of the amyloid precursor protein (APP) and methods of
CC      identifying those enzymes. The methods may be used to identify enzymes
CC      that may be used to cleave the alpha-secretase cleavage site of the APP
CC      protein. The enzymes may be used to treat or modulate the progress of
CC      Alzheimer's disease. The present sequence is human aspartyl protease 1
CC      (Asp 1) cDNA. Asp 1 has alpha-secretase protease and beta-secretase
CC      protease activities. Asp 1 gene is located on chromosome 21
XX
SQ      Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match          100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
      |||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
      |||
Db      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG 180
      |||
Db      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG 180

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCATG 240
      |||
Db      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCATG 240

Qy      241 GTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

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Db	241		GTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301		CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301		CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361		ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361		ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421		AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421		AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481		GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481		GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541		TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541		TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601		TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601		TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCGTGCT	720
Db	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCGTGCT	720
Qy	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781		GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781		GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021		CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021		CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140

Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

RESULT 6

AAS11516

ID AAS11516 standard; cDNA; 1804 BP.

XX

AC AAS11516;

XX

DT 24-OCT-2001 (first entry)  
 XX  
 DE Human cDNA encoding Aspartyl protease 1 (Asp1).  
 XX  
 KW Human; Aspartyl protease; Asp1; Asp2; beta-secretase; nootropic;  
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;  
 KW amyloid-beta; Abeta; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .1557  
 FT /\*tag= a  
 FT /product= "Asp1"  
 XX  
 PN WO200149098-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-502549/55.  
 DR P-PSDB; AAU06602.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 2; Fig 1; 185pp; English.  
 XX  
 CC The invention relates to a purified polypeptide comprising a fragment of  
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2  
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and  
 CC the fragment retain the beta-secretase activity of the mammalian Asp2  
 CC protein. The invention also details polynucleotides for the Asp proteins  
 CC and vectors expressing them, and a polypeptide (isoform of amyloid  
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or  
 CC its fragment containing an APP cleavage site recognizable by a mammalian  
 CC beta-secretase, and further comprising two lysine residues at the  
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP  
 CC fragment. Also included in the invention are methods of identifying  
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are  
 CC useful for treating Alzheimer's disease. APP is useful in methods for  
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-  
 CC beta (Abeta) peptide production. APP is also useful in designing  
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP

CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is  
CC associated with increased levels of Abeta processing is useful in assays  
CC relating the Alzheimer's research. The expression vector is useful for  
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp  
CC oligonucleotides are useful as probes or primers. The probes are useful  
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and  
CC Southern blots. The present sequence encodes human Asp1

XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACCTTCTTGCCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACCTTCTTGCCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660



Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500

```

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          |||
Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          |||
Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTCTTCAATCTCTGTTCT 1680
          |||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800

Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

```

RESULT 7

ABL52456

```

ID      ABL52456 standard; cDNA; 1804 BP.
XX
AC      ABL52456;
XX
DT      16-JUL-2002 (first entry)
XX
DE      Human Asp-1 nucleotide sequence SEQ ID NO:1.
XX
KW      Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
KW      proteolytic; chromosome 21; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key          Location/Qualifiers
FT      CDS          1..1557
FT                      /*tag= a
FT                      /product= "Asp-1"
FT                      /note= "aspartyl protease"
XX
PN      GB2367060-A.
XX
PD      27-MAR-2002.
XX
PF      29-OCT-2001; 2001GB-00025934.
XX
PR      23-SEP-1999; 99US-00404133.
PR      23-SEP-1999; 99US-0155493P.
PR      23-SEP-1999; 99WO-US020881.
PR      13-OCT-1999; 99US-00416901.
PR      06-DEC-1999; 99US-0169232P.

```

PR 22-SEP-2000; 2000GB-00023315.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Bienkowski MJ, Gurney M;  
 XX  
 DR WPI; 2002-397167/43.  
 DR P-PSDB; ABB78589.  
 XX  
 PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl  
 PT protease activity, e.g. for the diagnosis of Alzheimer's disease.  
 XX  
 PS Claim 8; Fig 1; 182pp; English.  
 XX  
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)  
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,  
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-  
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1  
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with  
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1  
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a  
 CC nucleotide sequence that hybridises under stringent conditions to the non  
 CC -coding strand complementary to a defined 1804 nucleotide sequence (see  
 CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1  
 CC proteolytic activity and lacks nucleotides encoding a transmembrane  
 CC domain); (3) a purified polynucleotide (III') comprising a sequence that  
 CC hybridises under stringent conditions to (III) (the nucleotide sequence  
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding  
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)  
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or  
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease  
 CC substrate (I) may be used as an enzyme substrate in assays to detect  
 CC aspartyl protease activity, (II) and therefore diagnose diseases  
 CC associated with aberrant hu-Asp1 expression and activity such as  
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while  
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present  
 CC sequence encodes hu-Asp1 from the present invention  
 XX  
 SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 6; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 60  
 Db 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 60

Qy 61 GCCCCGAGCTGGCCCCCGCGCCCTTACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
 Db 61 GCCCCGAGCTGGCCCCCGCGCCCTTACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy 121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG 180  
 Db 121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG 180

Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCAACTTCTTGCCATG 240

Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

RESULT 8  
AAZ34056

ID AAZ34056 standard; cDNA; 1879 BP.  
 XX  
 AC AAZ34056;  
 XX  
 DT 07-DEC-1999 (first entry)  
 XX  
 DE Human PRO852 nucleotide sequence.  
 XX  
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9946281-A2.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 08-MAR-1999; 99WO-US005028.  
 XX  
 PR 10-MAR-1998; 98US-0077450P.  
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PR 18-MAY-1998; 98US-0086023P.  
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PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.

XX

PA (GETH ) GENENTECH INC.

XX

PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX

DR WPI; 1999-551358/46.

DR P-PSDB; AAY41714.  
XX  
PT New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders.  
XX  
PS Claim 2; Fig 72; 530pp; English.  
XX  
CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to  
CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;

Query Match 98.9%; Score 1784.4; DB 2; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC	60
Db	94	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC	153
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573



Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380

Db	1414		GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGGTGTCAGCGTCGCCCC	1500
Db	1534		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGGTGTCAGCGTCGCCCC	1593
Qy	1501		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1680
Db	1714		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1773
Qy	1681		GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774		GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741		CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1786
Db	1834		CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1879

RESULT 9

AAC78500

ID AAC78500 standard; cDNA; 1879 BP.

XX

AC AAC78500;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human PRO852 (UNQ418) nucleotide sequence SEQ ID NO:195.

XX

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200053756-A2.

XX

PD 14-SEP-2000.

XX

PF 18-FEB-2000; 2000WO-US004341.

XX

PR 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.

PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX  
 DR WPI; 2000-611443/58.  
 DR P-PSDB; AAB44270.  
 XX  
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
 PT target bioactive molecules to specific cells, and to modulate cellular  
 PT activities.  
 XX  
 PS Claim 2; Fig 72; 636pp; English.  
 XX  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
 CC polynucleotides and polypeptides can be used for detecting the presence  
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
 CC and for modulating biological activities of cells, using the polypeptides  
 CC for specific targeting. The polypeptide targeting can be used to kill the  
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
 CC AAC78987 represent PCR primers and probes used in the isolation of the  
 CC PRO polynucleotide sequences  
 XX  
 SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;  
  
 Query Match 98.9%; Score 1784.4; DB 3; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 60  
 |  
 Db 94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 153  
  
 Qy 61 GCGCCGGAGCTGGCCCCCGCGCCCTTACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
 |  
 Db 154 GCGCCGGAGCTGGCCCCCGCGCCCTTACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGCGCCGCGCAACTTCTTGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGCGCCGCGCAACTTCTTGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCGTGGGATTAAATGGAATGGAATACCTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCGTGGGATTAAATGGAATGGAATACCTGGCCTAGCT	693
Qy	601	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053

Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAAATTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAAATTTCATTCTAA	1879

RESULT 10  
AAS45960  
ID AAS45960 standard; cDNA; 1879 BP.  
XX  
AC AAS45960;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human DNA encoding PRO polypeptide sequence #36.  
XX  
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;  
KW PCR primer.  
XX  
OS Homo sapiens.  
XX  
PN WO200168848-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 28-FEB-2001; 2001WO-US006520.  
XX  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 06-MAR-2000; 2000US-0186968P.  
PR 14-MAR-2000; 2000US-0189320P.  
PR 14-MAR-2000; 2000US-0189328P.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 21-MAR-2000; 2000US-0190828P.  
PR 21-MAR-2000; 2000US-0191007P.  
PR 21-MAR-2000; 2000US-0191048P.  
PR 21-MAR-2000; 2000US-0191314P.  
PR 28-MAR-2000; 2000US-0192655P.  
PR 29-MAR-2000; 2000US-0193032P.  
PR 29-MAR-2000; 2000US-0193053P.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 04-APR-2000; 2000US-0194449P.  
PR 04-APR-2000; 2000US-0194647P.  
PR 11-APR-2000; 2000US-0195975P.  
PR 11-APR-2000; 2000US-0196000P.  
PR 11-APR-2000; 2000US-0196187P.  
PR 11-APR-2000; 2000US-0196690P.  
PR 11-APR-2000; 2000US-0196820P.  
PR 18-APR-2000; 2000US-0198121P.  
PR 18-APR-2000; 2000US-0198585P.  
PR 25-APR-2000; 2000US-0199397P.  
PR 25-APR-2000; 2000US-0199550P.  
PR 25-APR-2000; 2000US-0199654P.  
PR 03-MAY-2000; 2000US-0201516P.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.

PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-602746/68.  
 DR P-PSDB; AAU29059.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX  
 PS Claim 2; Fig 71; 774pp; English.  
 XX  
 CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
 CC primers for PRO polypeptides of the invention. The sequences of the  
 CC invention can be used to detect the presence of a tumour in a mammal by  
 CC comparing the level of expression of a PRO polypeptide in a test sample  
 CC of cells from the animal and a control sample of normal cells, whereby a  
 CC higher level of expression in the test sample indicates the presence of a  
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
 CC blood, when contacted with it. A specific polypeptide can be used to  
 CC stimulate the proliferation or differentiation of chondrocyte cells. The  
 CC PRO proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX  
 SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;  
  
 Query Match 98.9%; Score 1784.4; DB 4; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 60  
 Db 94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC 153  
  
 Qy 61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
 Db 154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213  
  
 Qy 121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
 Db 214 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273  
  
 Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACCTTCTTGCCCATG 240

Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080



Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1879

RESULT 11

ABX78563

ID ABX78563 standard; cDNA; 1879 BP.

XX

AC ABX78563;

XX

DT 15-APR-2003 (first entry)  
XX  
DE Human PRO polynucleotide #36.  
XX  
KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;  
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003027272-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 21-JUN-2002; 2002US-00176492.  
XX  
PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
PR 28-OCT-1997; 97US-0063540P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063734P.  
PR 31-OCT-1997; 97US-0063870P.  
PR 31-OCT-1997; 97US-0064103P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 17-DEC-1997; 97US-0069870P.  
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PR 10-MAR-1998; 98US-0077450P.  
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ACA75535

ID ACA75535 standard; cDNA; 1879 BP.

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DT 07-JUL-2003 (first entry)

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DE Novel human secreted and transmembrane protein PRO852 cDNA.

XX

KW Human; secreted and transmembrane protein: PRO; gene therapy;

KW tumour necrosis factor-alpha release; TNF-alpha release;

KW chondrocyte proliferation; chondrocyte differentiation; tumour;

KW adrenal tumour; lung tumour; colon tumour; breast tumour;

KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003032127-A1.

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Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
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RESULT 13

ACA71015

ID ACA71015 standard; cDNA; 1879 BP.

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AC ACA71015;

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DT 02-AUG-2003 (first entry)

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DE Human secreted/transmembrane protein (PRO) cDNA #36.

XX

KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;  
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
 KW tissue typing.

XX

OS Homo sapiens.

XX

PN US2003032112-A1.

XX

PD 13-FEB-2003.

XX

PF 21-JUN-2002; 2002US-00176756.

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Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;



Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
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Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
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Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
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Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933

Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
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Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
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Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
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Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
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QY 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
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RESULT 14

ACC87543

ID ACC87543 standard; cDNA; 1879 BP.

XX

AC ACC87543;

XX

DT 05-AUG-2003 (first entry)

XX

DE Human secreted polypeptide PRO852-encoding cDNA, SEQ ID NO:71.

XX

KW Human; PRO; secreted protein; transmembrane protein;

KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;

KW chondrocyte; proliferation; differentiation; cartilage disorder;

KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;

KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;

KW liver; drug screening; transgenic animal; genetic analysis;

KW antiarthritic; vulnerary; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003027278-A1.

XX

PD 06-FEB-2003.

XX

PF 21-JUN-2002; 2002US-00176987.

XX

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

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Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	120
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Qy	121	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273

Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
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Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
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Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
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Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
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Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Db	1114		CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174		TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCA	1200
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Qy	1261		AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
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Qy	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1533
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RESULT 15

ACC86929

ID ACC86929 standard; cDNA; 1879 BP.

XX

AC ACC86929;



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 DT 05-AUG-2003 (first entry)  
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 XX  
 KW Human; PRO; secreted protein; transmembrane protein;  
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
 KW chondrocyte; proliferation; differentiation; cartilage disorder;  
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
 KW liver; drug screening; transgenic animal; genetic analysis;  
 KW antiarthritic; vulnerary; gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036159-A1.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 02-JUL-2002; 2002US-00188773.  
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 PR 18-SEP-1997; 97US-0059263P.  
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Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
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Job time : 710 secs

OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 18:32:27 ; Search time 154 Seconds  
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Total number of hits satisfying chosen parameters: 1365418

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1804	100.0	1804	4	US-09-548-367D-1	Sequence 1, Appli
3	1804	100.0	1804	4	US-09-551-853D-1	Sequence 1, Appli
4	1768.2	98.0	1873	4	US-09-215-450-18	Sequence 18, Appl
5	1765.6	97.9	1862	3	US-08-999-723-1	Sequence 1, Appli
6	1765.6	97.9	1862	3	US-09-434-427-1	Sequence 1, Appli
7	1478.6	82.0	2429	4	US-09-215-450-1	Sequence 1, Appli
8	1134.2	62.9	1545	3	US-09-717-432-1	Sequence 1, Appli
9	1134.2	62.9	1545	4	US-09-912-484-1	Sequence 1, Appli
10	1104.6	61.2	2514	4	US-09-280-116-32	Sequence 32, Appl
11	953.6	52.9	1021	4	US-09-280-116-85	Sequence 85, Appl

12	397.4	22.0	2348	4	US-09-724-566A-42	Sequence 42, Appl
13	397.4	22.0	2348	4	US-09-724-566A-44	Sequence 44, Appl
14	397.4	22.0	16080	4	US-09-724-566A-48	Sequence 48, Appl
15	395	21.9	1503	4	US-09-724-566A-1	Sequence 1, Appli
16	395	21.9	2070	4	US-09-548-372D-3	Sequence 3, Appli
17	395	21.9	2070	4	US-09-548-367D-3	Sequence 3, Appli
18	395	21.9	2070	4	US-09-551-853D-3	Sequence 3, Appli
19	395	21.9	3252	4	US-09-604-608-1	Sequence 1, Appli
20	393.4	21.8	2541	4	US-09-009-191-1	Sequence 1, Appli
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22	386	21.4	1380	4	US-09-548-372D-23	Sequence 23, Appl
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24	386	21.4	1380	4	US-09-551-853D-23	Sequence 23, Appl
25	385	21.3	1362	4	US-09-548-372D-29	Sequence 29, Appl
26	385	21.3	1362	4	US-09-548-367D-29	Sequence 29, Appl
27	385	21.3	1362	4	US-09-551-853D-29	Sequence 29, Appl
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41	380.8	21.1	1278	4	US-09-548-372D-27	Sequence 27, Appl
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#### ALIGNMENTS

##### RESULT 1

US-09-548-372D-1

; Sequence 1, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23



; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-548-372D-1

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
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Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660

Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTGAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Db	1141	ATTGAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500

Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

RESULT 2

US-09-548-367D-1

; Sequence 1, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1804

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-548-367D-1

Query Match	100.0%;	Score 1804;	DB 4;	Length 1804;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1804;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps
			0;	

Qy	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900

Db	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021		CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021		CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261		AGAGCCCGAGAAGAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261		AGAGCCCGAGAAGAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321		GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321		GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501		CGTGACCCTGAGGTTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501		CGTGACCCTGAGGTTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681		GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740

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Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAAAA 1800
Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

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RESULT 3

US-09-551-853D-1

; Sequence 1, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1804

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-551-853D-1

Query Match 100.0%; Score 1804; DB 4; Length 1804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          |||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
Qy      61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          |||
Db      61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
Qy      121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          |||
Db      121 CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG 240
          |||

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Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
Qy	241	G TAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	G TAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACCTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACCTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 4  
 US-09-215-450-18  
 ; Sequence 18, Application US/09215450



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; Patent No. 6635748
; GENERAL INFORMATION:
; APPLICANT: Giese, Klaus
; APPLICANT: Xin, Hong
; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES
; FILE REFERENCE: 1451.100 / 210030.447
; CURRENT APPLICATION NUMBER: US/09/215,450
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: human
US-09-215-450-18

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Query Match          98.0%; Score 1768.2; DB 4; Length 1873;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 220

Qy     121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 340

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 520

Qy     421 AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     521 AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     581 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 640

Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

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Db	641	 TTGGAATCAGAGAATTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	700
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	701	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	760
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	761	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	820
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	821	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	880
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	881	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	940
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	941	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1000
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1001	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1060
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1061	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1120
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1121	 CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1180
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTTCATTCCGTATCACAACTCCTGCCTCAGCTTTAC	1140
Db	1181	 TACCTGAGAGATGAGAACTCCAGCAGGTTCATTCCGTATCACAACTCCTGCCTCAGCTTTAC	1240
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1241	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1300
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1301	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1360
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1361	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1420
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1421	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1480
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

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Db      1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCATGCGCTCATGAGCGTCTGTGGA 1540
QY      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1500
          |||
Db      1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1600
QY      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          |||
Db      1601 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1660
QY      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          |||
Db      1661 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1720
QY      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTTCAATCTCTGTTCT 1680
          |||
Db      1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTTCAATCTCTGTTCT 1780
QY      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1781 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840
QY      1741 CTCCCTACTTCCAAGAAAAATAATTAATAAAAAA 1773
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Db      1841 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAA 1873

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# RESULT 5

US-08-999-723-1

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; Sequence 1, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASPl
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-999-723-1

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Query Match          97.9%; Score 1765.6; DB 3; Length 1862;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1768; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCC 60
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Db      91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCC 150
QY      61 GCGCCGGAGCTGGCCCCCGCGCCCTTACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

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Db	151	 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	210
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	211	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	270
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	271	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	330
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	331	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	390
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	391	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	450
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	451	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	510
Qy	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	511	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	570
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	571	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	630
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	631	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	690
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	691	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	750
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	751	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	810
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	811	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	870
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	871	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	930
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	931	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	990
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960

Db	991	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAAGGTGTTTGATGCGGTGGTG	1050
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1051	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1110
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1111	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1170
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1171	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1230
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Db	1231	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1290
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1291	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1350
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1351	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1410
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1411	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1470
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1471	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1530
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1531	GCCATCCTCCTTGTCTTAATCGTCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1590
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1591	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1650
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1651	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1710
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1711	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1770
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1771	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1830
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAA	1772
Db	1831	CTCCCTACTTCCAAGAAAAATAATTAAAAAA	1862

RESULT 6  
 US-09-434-427-1  
 ; Sequence 1, Application US/09434427  
 ; Patent No. 6162630  
 ; GENERAL INFORMATION:  
 ; APPLICANT: POWELL, DAVID J.  
 ; APPLICANT: SOUTHAN, CHRISTOPHER  
 ; APPLICANT: CHAPMAN, CONRAD G.  
 ; APPLICANT: EVANS, JOANNE R.  
 ; TITLE OF INVENTION: ASP1  
 ; FILE REFERENCE: GH-70262-D1  
 ; CURRENT APPLICATION NUMBER: US/09/434,427  
 ; CURRENT FILING DATE: 1999-11-04  
 ; EARLIER APPLICATION NUMBER: US 08/999,723  
 ; EARLIER FILING DATE: 1997-10-06  
 ; EARLIER APPLICATION NUMBER: UK 9626022.9  
 ; EARLIER FILING DATE: 1996-12-14  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1862  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-09-434-427-1

Query Match 97.9%; Score 1765.6; DB 3; Length 1862;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1768; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	91	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	150
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	151	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	210
Qy	121	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	211	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	270
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
Db	271	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	330
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	331	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	390
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	391	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	450
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420

Db	451	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	510
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	511	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	570
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	571	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	630
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	631	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	690
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	691	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	750
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCC GTTGCT	720
Db	751	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCC GTTGCT	810
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	811	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	870
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTGAAA	840
Db	871	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTGAAA	930
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	931	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	990
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	991	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1050
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1051	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1110
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1111	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1170
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1140
Db	1171	TACCTGAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1230
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1231	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1290
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1291	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1350

Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1351	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1410
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1411	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1470
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1471	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1530
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1531	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1590
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1591	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1650
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1651	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1710
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1711	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1770
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1771	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1830
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAA	1772
Db	1831	CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAAAAA	1862

# RESULT 7

US-09-215-450-1

; Sequence 1, Application US/09215450

; Patent No. 6635748

; GENERAL INFORMATION:

; APPLICANT: Giese, Klaus

; APPLICANT: Xin, Hong

; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES

; FILE REFERENCE: 1451.100 / 210030.447

; CURRENT APPLICATION NUMBER: US/09/215,450

; CURRENT FILING DATE: 1998-12-17

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2429

; TYPE: DNA

; ORGANISM: human

US-09-215-450-1







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; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: MUS MUSCULUS
US-09-717-432-1

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Query Match          62.9%; Score 1134.2; DB 3; Length 1545;
Best Local Similarity 83.6%; Pred. No. 5.5e-260;
Matches 1302; Conservative 0; Mismatches 243; Indels 12; Gaps 1;

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Qy      1 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db      1 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCTTGAGTGCG 60

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
        | ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCAAGTGGCCGGGGCCACGAAC 120

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
        | | || || || || || || || || || || || || || || ||
Db    121 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCGAGTTGCCCCGGGCCGATGGTCTG 180

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGCCCATG 240
        || |||| | ||||| || | ||| | ||||| ||||| |||
Db    181 GCCCTCGCACTGGAGCCTGTCAGGGC-----TACTGCCAACTTCTTGCTATG 228

Qy    241 GTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    229 GTGGACAACCTTCAGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 288

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    289 CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT 348

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
        |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    349 GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC 408

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
        ||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||
Db    409 AAGGGCTTTGATGTCACTGTGAAGTACACACAGGAAGCTGGACTGGCTTTGTTGGTGAG 468

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
        |||| | ||||| ||||| ||||| |||| | |||| | ||||| |||||
Db    469 GACCTTGTCAACCATCCCCAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT 528

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db    529 TTCGAGTCTGAGAATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT 588

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Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	589	TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTTGATTCCCTGGTGGCC	648
Qy	661	CAAGCAAACATCCCCAACGTTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCGTGCT	720
Db	649	CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT	708
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	709	GGTTCTGGTACCAACGGAGGTAGTCTTGTCTTGGGTGGGATTGAACCAAGTTTGTATAAA	768
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	769	GGAGATATCTGGTATACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG	828
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	829	TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	888
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	889	ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG	948
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	949	GAAGCTGTGGCACCAGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC	1008
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1009	CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTCTATC	1068
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1069	TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCACAGCTCTAC	1128
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCCCA	1200
Db	1129	ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTGGTATCTCCTCT	1188
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1189	TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC	1248
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1249	AGAGCTCAGAGGAGGGTGGGCTTTCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA	1308
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1309	GTGTCTGAAATTTCTGGGCCCTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCA	1368
Qy	1381	CAGTCTTTGAGCGAGCCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1369	CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCTATGCCCTGATGAGTGTGTGTGGA	1428

Qy	1	ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCTTGAGTGCG	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCAAGTGGCCGGGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCGAGTTGCCCCGGGGCCGATGGTCTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG	240
Db	181	GCCCTCGCACTGGAGCCTGTCAGGGC-----TACTGCCAACTTCTTGGCTATG	228
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	229	GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC	288

Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	289	CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT	348
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	349	GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC	408
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	409	AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG	468
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	469	GACCTTGTCAACCATCCCCAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT	528
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	529	TTGAGTCTGAGAATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT	588
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	589	TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGTATCCCTGGTGGCC	648
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	649	CAAGCAAAGATTCCAGACATTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT	708
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	709	GGTTCCTGGTACCAACGGAGGTAGTCTTGTCTTGGGTGGGATTGAACCAAGTTTGTATAAA	768
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCGTAAA	840
Db	769	GGAGATATCTGGTATACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG	828
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	829	TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	888
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	889	ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCACTGGTG	948
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	949	GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTCTGATGGCTTCTGGACAGGGGCC	1008
Qy	1021	CAGCTGGCGTGCTGGACGAATTCCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1009	CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC	1068
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1069	TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCACAGCTCTAC	1128

Qy	1141	ATTCAGCCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCCA	1200
Db	1129	ATTCAGCCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT	1188
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1189	TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC	1248
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1249	AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA	1308
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1309	GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCA	1368
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1369	CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGGA	1428
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCGGTGTCAGCGTCGCCCC	1500
Db	1429	GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCCTGCACTGCCGTTCATGCCCC	1488
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA	1557
Db	1489	CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA	1545

US-09-280-116-32

; Patent No. 6331427

; APPLICANT: Robison, Keith E.

; FILE REFERENCE: 5800-24, 035800/176965

; CURRENT FILING DATE: 1999-03-26

; SOFTWARE: PatentIn Ver. 2.0

; LENGTH: 2514

; ORGANISM: Homo sapiens

; OTHER INFORMATION: aspartyl proteases

Query Match 61.2%; Score 1104.6; DB 4; Length 2514;

Matches 1428; Conservative 0; Mismatches 64;

Qy 305 CGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAAC TTTGCCGTGGCAGGAACCC 364  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 213 CTCACCAGCTACAGATTCTCGTTGACACTGGAAGCAGTAAC TTTGCCGTGG-AGGAACCC 271

Qy	365	CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG	424
Db	272	CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG	331
Qy	425	GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC	484
Db	332	GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC	391
Qy	485	TCGTCACCATCCCCAAAGGCTTC-AATACTTCTTTTCTTGTCAACATTGCCACTATTTTT	543
Db	392	TCGTCACCATCCCCAAAGGCTTCAAATACTTCTTTTCTTGTCAACATTGCCACTATTTTT	451
Qy	544	GAATCAGA-GAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA	602
Db	452	GAATCAGAGGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA	511
Qy	603	TGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTG---AC	659
Db	512	TGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGAACAC	571
Qy	660	ACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCC-GGCTTGCCCGTTG	718
Db	572	AAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGGCTTGCCCGTTG	631
Qy	719	CTGG-----ATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT	773
Db	632	GCTGGGATCTGGGGAACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT	691
Qy	774	GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT	833
Db	692	GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT	751
Qy	834	TCTGAAATT---GGAAATTGGAGGCCAAAGCCTTAAT-----CTGGACTGCAGAGAGTA	884
Db	752	TCTTGAAATTGGGAAATTGGGAGGCCAAAGCCTTAATCTTGGGACTGCAGGAGGAGTAT	811
Qy	885	TAACGCAGACAAGG--CCATCGTGGACAGT-GGCACCACGCTGCTGCGCCT--GCCCCAG	939
Db	812	TAACGCAGACAAGGGCCATCGTTGGACAGTGGGCACCACGCTGCTGCGCCTTGCCCCAG	871
Qy	940	AAGGTGTTTGATGCGGTGGT-GGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC	998
Db	872	AAGGTGTTTGATGCGGTGGTGGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC	931
Qy	999	TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTC	1058
Db	932	TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTC	991
Qy	1059	TTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTAT	1118
Db	992	TTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCAATCCGTAT	1051
Qy	1119	CACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGGCGGCCTGAATTATGAATG	1178
Db	1052	CACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGGCGGCCTGAATTATGAATG	1111
Qy	1179	TTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA	1238



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      |||
Db      1112 TTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA 1171
Qy      1239 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1298
      |||
Db      1172 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1231
Qy      1299 TGCAGAAATTGCA-GGTGCTGC-AGTGTCTGAAATTTCCGGGCCTTTCTC-AACAGAGGA 1355
      |||
Db      1232 TGCAGAAATTGCACGGTGCTGCAAGTGTCTGAAATTTCCGGGCCTTTCTCAAACAGAGGA 1291
Qy      1356 TGTAGCCAG-CAACTGTGTCCCCGCTC-AGTCTTTGAGCGA-GCCCATTTTGTGGATTGT 1412
      |||
Db      1292 TGTAGCCAGCCAACTGTGTCCCCGCTCAAGTCTTTGAGCGACGCCCATTTTGTGGATTGT 1351
Qy      1413 GTCC----TATGCGCTCATGAGCGTCTGTGG-AGCCATCCTCCTTGTC-TTAATCGTCCT 1466
      |||
Db      1352 GTCCCTATGCCGCTCAATGAAGCGTCTGTGGAAGCCATCCTCCTTGTCGTTAATTCAAGTC 1411
Qy      1467 GCTGCTGC----TGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1522
      |||
Db      1412 GCTGCTGCTGCTTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1471
Qy      1523 ATGAGTCCTCTCT-GGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1581
      |||
Db      1472 ATGAGTCCTCTCTGGGTGAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1531
Qy      1582 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1641
      |||
Db      1532 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1591
Qy      1642 CGCTTTCTCCTGTGCCCACCCGCTCTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGAT 1701
      |||
Db      1592 CGCTTTCTCCTGTGCCCACCCGCTCTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGAT 1651
Qy      1702 TCACTGTCTTTTGATTCTTGATTTTCAAGC-TTTCAAATCCTCCCTACTTCCAAGAAAAA 1760
      |||
Db      1652 TCACTGTCTTTTGATTCTTGATTTTCAAGCTTTTCAAATCCTCCCTACTTCCAAGAAAAA 1711
Qy      1761 TAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAA 1797
      |||
Db      1712 TAATTAAAAAAAAAACTTCATTCTAAACCAAAACAGA 1748

```

RESULT 11

US-09-280-116-85

; Sequence 85, Application US/09280116A

; Patent No. 6331427

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs

; FILE REFERENCE: 5800-24, 035800/176965

; CURRENT APPLICATION NUMBER: US/09/280,116A

; CURRENT FILING DATE: 1999-03-26

; NUMBER OF SEQ ID NOS: 268

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 85

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; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: aspartyl proteases
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1021)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-85
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Query Match          52.9%; Score 953.6; DB 4; Length 1021;
Best Local Similarity 98.8%; Pred. No. 3.7e-217;
Matches 971; Conservative 0; Mismatches 10; Indels 2; Gaps 1;
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Qy      98 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTG 157
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGAGCCCTG 97

Qy     158 CCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG 217
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 CCGAGCGCCACGCCGACGGCTNGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG 157

Qy     218 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 277
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 217

Qy     278 ACCTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 337
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 ACCTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 277

Qy     338 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 397
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 337

Qy     398 AGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 457
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 AGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 397

Qy     458 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 517
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 457

Qy     518 TTCTTGTCAACATTGCCACTATTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAAT 577
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 TTCTTGTCAACATTGCCACTATTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAAT 517

Qy     578 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 637
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     518 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 577

Qy     638 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 697
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     578 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 637

Qy     698 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 757
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 638 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 697  
 Qy 758 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 817  
 Db 698 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 755  
 Qy 818 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 877  
 Db 758 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 817  
 Qy 878 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 937  
 Db 818 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 877  
 Qy 938 AGAAGGTGTTTGATGC--GGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 995  
 Db 878 AGAAGGTGTTTGATGCCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 937  
 Qy 996 CTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTTCGGAAACACCTTG 1055  
 Db 938 CTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTTCGGAAACACCTTG 997  
 Qy 1056 GTCTTACTTCCCTAAAATCTCCA 1078  
 Db 998 GTCTTACTTCCCTAAAATCTTCA 1020

RESULT 12

US-09-724-566A-42

; Sequence 42, Application US/09724566A

; Patent No. 6627739

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, No. 6627739mand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; TITLE OF INVENTION: Methods

; FILE REFERENCE: 228-US-NEWC2

; CURRENT APPLICATION NUMBER: US/09/724,566A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/501,708

; PRIOR FILING DATE: 2000-02-10

; PRIOR APPLICATION NUMBER: 60/119,571

; PRIOR FILING DATE: 1999-02-10

; PRIOR APPLICATION NUMBER: 60/139,172

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 42

; LENGTH: 2348  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-566A-42

Query Match 22.0%; Score 397.4; DB 4; Length 2348;  
Best Local Similarity 55.0%; Pred. No. 7.1e-85;  
Matches 863; Conservative 0; Mismatches 676; Indels 30; Gaps 3;

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Qy      2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      238 TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCAGAGCCAGAGGGCCGAAGGCCGG 297

Qy      62 CCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAACC 121
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      298 GGCCCAACATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 357

Qy     122 GCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     358 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCC 417

Qy     182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGGCGCCGC----- 224
      | | | | | | | | | | | | | | | | | | | | | | | |
Db     418 CCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 477

Qy     225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     478 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 537

Qy     284 AGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
      |||| | | | | | | | | | | | | | | | | | | | | | |
Db     538 AGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGCTGATACAGGCAGCAGTA 597

Qy     344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
      ||||| ||| | | | | | | | | | | | | | | | | | | |
Db     598 ACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 657

Qy     404 CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGA 463
      | ||||| ||| | | | | | | | | | | | | | | | | | |
Db     658 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 717

Qy     464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
      || | | | | | | | | | | | | | | | | | | | | | |
Db     718 AAGGGGAGCTGGGCACCGACCTGCTAAGCATCCCCCATGGCCCCAACGTCAGTGTGCGTG 777

Qy     524 TCAACATTGCCACTATTTTGAATCAGAGAATTCTTTTGCCTGGGATTAAATGGAATG 583
      ||||| ||| | | | | | | | | | | | | | | | | | |
Db     778 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAG 837

Qy     584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
      | | | | | | | | | | | | | | | | | | | | | | |
Db     838 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 897

Qy     644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
      | ||||| ||| | | | | | | | | | | | | | | | | | |
Db     898 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 957
```

Qy 704 CCGGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 958 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTG 1017  
 Qy 755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1018 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 1077  
 Qy 815 GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1078 GGTATTATGAGGTGATCATTTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 1137  
 Qy 875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1138 GCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 1197  
 Qy 935 CCCAGAAGGTGTTTGTATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1198 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 1257  
 Qy 995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1258 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 1317  
 Qy 1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1318 GGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 1377  
 Qy 1115 GTATCACAATCCTGCCTCAGCTTTACATTGAGCCCATGATGGGGGCCGCTG---AATT 1171  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1378 GCATCACCATCCTTCCGAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCCAAG 1437  
 Qy 1172 ATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1438 ACGACTGTTACAAGTTTGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 1497  
 Qy 1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1498 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCA 1557  
 Qy 1292 GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCCTTTCTCAACAG 1351  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1558 GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCT 1617  
 Qy 1352 AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1618 TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 1677  
 Qy 1412 TGTCCATATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471  
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 Db 1678 TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 1737  
 Qy 1472 TGCTGCCGTTCCGGTGTACGCTCGCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531  
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 Db 1738 GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 1797  
 Qy 1532 CTCTGGTCA 1540

Db 1798 CCCTGCTGA 1806

RESULT 13  
US-09-724-566A-44  
; Sequence 44, Application US/09724566A  
; Patent No. 6627739  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, John P.  
; APPLICANT: Basi, Guriqbal  
; APPLICANT: Doane, Minh Tam  
; APPLICANT: Frigon, No. 6627739mand  
; APPLICANT: John, Varghese  
; APPLICANT: Power, Michael  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Tatsuno, Gwen  
; APPLICANT: Tung, Jay  
; APPLICANT: Wang, Shuwen  
; APPLICANT: McConlogue, Lisa  
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: 228-US-NEWC2  
; CURRENT APPLICATION NUMBER: US/09/724,566A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/501,708  
; PRIOR FILING DATE: 2000-02-10  
; PRIOR APPLICATION NUMBER: 60/119,571  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/139,172  
; PRIOR FILING DATE: 1999-06-15  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 2348  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-566A-44

Query Match 22.0%; Score 397.4; DB 4; Length 2348;  
Best Local Similarity 55.0%; Pred. No. 7.1e-85;  
Matches 863; Conservative 0; Mismatches 676; Indels 30; Gaps 3;

Qy	2	TGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCCAGTGGCTCCTGCGCGCCG	61
Db	238	TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCCGAAGGCCGG	297
Qy	62	CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAACC	121
Db	298	GGCCCACCATGGCCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC	357
Qy	122	GCGTAGTTGCGCCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG	181
Db	358	CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCC	417
Qy	182	CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGC-----	224

Db 418 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCCGGCCGGAGGG 477  
 Qy 225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283  
 || ||| ||| ||||| ||||| ||| | || || | ||||| |||  
 Db 478 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 537  
 Qy 284 AGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343  
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 Db 538 AGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 597  
 Qy 344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403  
 ||||| |||| | |||| ||| ||| | | |||| | | || ||  
 Db 598 ACTTTGCAGTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGT 657  
 Qy 404 CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGA 463  
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 Db 658 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 717  
 Qy 464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523  
 || || || ||||| || | ||||| || || || || || || || ||  
 Db 718 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 777  
 Qy 524 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATG 583  
 ||||| || || ||||| || ||||| | || || || || || ||  
 Db 778 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAATGGGAAG 837  
 Qy 584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643  
 | || || || || || ||||| ||||| || || ||||| | |||||  
 Db 838 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 897  
 Qy 644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAG 703  
 | |||| |||| | || | || | ||||| ||||| ||||| |||||  
 Db 898 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 957  
 Qy 704 CCGGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754  
 | |||| ||| | || | | ||||| || | || || ||  
 Db 958 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTG 1017  
 Qy 755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814  
 | || || || | |||| ||| ||||| ||||| || || || || ||  
 Db 1018 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 1077  
 Qy 815 GGTACTACCAGATAGAAATCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874  
 |||| || || | || || |||| || || || || || || |||||  
 Db 1078 GGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 1137  
 Qy 875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934  
 ||| |||| ||| ||||| || ||||| ||||| ||||| || || ||  
 Db 1138 GCAAGGAGTACAACATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 1197  
 Qy 935 CCCAGAAGGTGTTTGTATGCGGTGGTGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994  
 || |||| ||||| || | || || | | || || || || || ||  
 Db 1198 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 1257  
 Qy 995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054  
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 Db 1258 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 1317





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; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 16080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression Vector pCEK
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(16080)
; OTHER INFORMATION: n = A,T,C or G
US-09-724-566A-48

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Query Match          22.0%;  Score 397.4;  DB 4;  Length 16080;
Best Local Similarity 55.0%;  Pred. No. 1.5e-84;
Matches 863;  Conservative 0;  Mismatches 676;  Indels 30;  Gaps 3;

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Qy      2  TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCCG 61
      |||| |||  ||| |||  |  ||| |||  ||||| ||  ||  |  ||
Db      1607 TGGGGGCGAGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCCG 1666

Qy      62  CCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAACC 121
      ||  ||||| ||  |  ||| |  || ||| |||||  |  |
Db      1667 GGCCCAACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 1726

Qy      122 GCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
      |  |  ||  |  ||  |  ||  ||  ||  ||  ||  ||  ||
Db      1727 CTGCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCCTGGGGGGCGCCC 1786

Qy      182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC----- 224
      ||| |  ||| ||  ||| ||| ||| ||  ||  |||
Db      1787 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 1846

Qy      225 -CAACTTCTTGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
      || ||| |||  ||||  ||||| ||| ||| ||  ||||| |||
Db      1847 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 1906

Qy      284 AGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
      |||||  |  ||  ||||| ||||| |||  |  ||  ||  ||  ||  ||  ||
Db      1907 AGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 1966

Qy      344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
      ||||| ||||  |  |||| ||| |||  |  |  ||||  |  ||  ||
Db      1967 ACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 2026

Qy      404 CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
      |  ||||| ||||  |  |  ||  |||  ||||  ||  ||  ||
Db      2027 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCAAGGCAAGTGGG 2086

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Qy	464	CGGGCTTCGTTGGGGAAGACCTTGTCCATCCCACCAAGGCTTCAATACTTCTTTTCTTG	523
Db	2087	AAGGGGAGCTGGGCACCACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTG	2146
Qy	524	TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATG	583
Db	2147	CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACGGGAAG	2206
Qy	584	GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT	643
Db	2207	GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT	2266
Qy	644	TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG	703
Db	2267	TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG	2326
Qy	704	CCGGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG	754
Db	2327	CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTG	2386
Qy	755	GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT	814
Db	2387	GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT	2446
Qy	815	GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT	874
Db	2447	GGTATTATGAGGTCATCATTTGTGCGGGTGAGATCAATGGACAGGATCTGAAAATGGACT	2506
Qy	875	GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACACGCTGCTGCGCCTGC	934
Db	2507	GCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCAACCTTCGTTTGC	2566
Qy	935	CCCAGAAGGTGTTTGATGCGGTGGTGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT	994
Db	2567	CCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT	2626
Qy	995	TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAACACCTT	1054
Db	2627	TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT	2686
Qy	1055	GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCAATTCC	1114
Db	2687	GGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC	2746
Qy	1115	GTATCACAATCCTGCCTCAGCTTTACATTACAGCCCATGATGGGGGCCGGCCTG---AATT	1171
Db	2747	GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGAAGATGTGGCCACGTCCCAAG	2806
Qy	1172	ATGAATGTTACCGATTTCGGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG	1231
Db	2807	ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA	2866
Qy	1232	TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA	1291
Db	2867	TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCA	2926

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Qy      1292  GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
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Db      2927  GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCT 2986

Qy      1352  AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
          || | | | | | | | | | | | | | | | |
Db      2987  TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 3046

Qy      1412  TGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
          | | | | | | | | | | | | | | | | | |
Db      3047  TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGGTGT 3106

Qy      1472  TGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCCTGAGGTCGTCAATGATGAGTCCT 1531
          | | | | | | | | | | | | | | | | | |
Db      3107  GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 3166

Qy      1532  CTCTGGTCA 1540
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Db      3167  CCCTGCTGA 3175

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RESULT 15

US-09-724-566A-1

; Sequence 1, Application US/09724566A

; Patent No. 6627739

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurqbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, No. 6627739mand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; TITLE OF INVENTION: Methods

; FILE REFERENCE: 228-US-NEWC2

; CURRENT APPLICATION NUMBER: US/09/724,566A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/501,708

; PRIOR FILING DATE: 2000-02-10

; PRIOR APPLICATION NUMBER: 60/119,571

; PRIOR FILING DATE: 1999-02-10

; PRIOR APPLICATION NUMBER: 60/139,172

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1503

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-566A-1

Query Match

21.9%; Score 395; DB 4; Length 1503;

Best Local Similarity 55.6%; Pred. No. 2.2e-84;  
Matches 805; Conservative 0; Mismatches 630; Indels 12; Gaps 2;

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Qy      106 GCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGC 165
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Db      55  GCCCACGGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCC 114

Qy      166 CACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCC 225
      | |  |  | |||  | |  ||  |  |  |  |  |||  |  |  |
Db      115 CTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGAGAGCCCGGCCGGAGGGGC 174

Qy      226 AACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG 285
      | |||  |||  ||||  |||||  |||||  |||  |  ||  |  |||||  |||||
Db      175 AGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAG 234

Qy      286 ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAAC 345
      |||  |  ||  | |||||  ||||  |||  |  ||  ||  ||  ||  |||||
Db      235 ATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAAC 294

Qy      346 TTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCT 405
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Db      295 TTTGCAGTGGGTGCTGCCCCCACCCTTCTCGCATCGTACTACCAGAGGCAGCTGTCC 354

Qy      406 AGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG 465
      |||||  ||||  |  |  |  ||  ||  ||  |||  ||||  ||  ||  |||
Db      355 AGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAA 414

Qy      466 GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC 525
      ||  |  ||  ||||  ||  |||||  ||  |||  |||  ||  ||  ||  ||
Db      415 GGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCAGTGTGCGTGCC 474

Qy      526 AACATTGCCACTATTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGA 585
      |||||  ||  ||  |||||  ||  |||||  ||  ||  ||  ||  ||  ||  ||
Db      475 AACATTGCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGC 534

Qy      586 ATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTC 645
      ||  ||  ||  ||  ||  ||||  |||||  |||  ||  |||||  ||  |||||
Db      535 ATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCCTGACGACTCCCTGGAGCCTTTCTTT 594

Qy      646 GACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAGCC 705
      ||||  ||||  |  ||  |  ||  ||  |||||  ||  |||||  ||||  ||  |||||
Db      595 GACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTGTGGTGCT 654

Qy      706 GGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGT 756
      ||||  |||  |  ||  |  |  |  ||||  ||  |  ||  ||
Db      655 GGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGA 714

Qy      757 GGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGG 816
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Db      715 GGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGG 774

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      ||  ||  ||  |  ||  ||  ||||  ||  ||  ||  ||  |||||
Db      775 TATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGC 834

Qy      877 AGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCC 936
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Qy	997	TCTGATGGTTCCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGG	1056
Db	955	CCTGATGGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGG	1014
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Qy	1234	ATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC	1293
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Db	1315	GACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATA	1374
Qy	1414	TCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTG	1473
Db	1375	GCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGTGCCACTCTGCCCTCATGGTGTGT	1434
Qy	1474	CTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCT	1533
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Job time : 161 secs

OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 23:19:02 ; Search time 654 Seconds  
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10088.696 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1804	100.0	1804	9	US-09-795-847-1	Sequence 1, Appli
3	1804	100.0	1804	9	US-09-794-743-1	Sequence 1, Appli
4	1804	100.0	1804	9	US-09-794-748-1	Sequence 1, Appli
5	1804	100.0	1804	9	US-09-794-925-1	Sequence 1, Appli
6	1804	100.0	1804	9	US-09-681-442-1	Sequence 1, Appli
7	1804	100.0	1804	10	US-09-869-414-1	Sequence 1, Appli
8	1804	100.0	1804	10	US-09-548-366-1	Sequence 1, Appli
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#### ALIGNMENTS

RESULT 1  
 US-09-794-927-1  
 ; Sequence 1, Application US/09794927  
 ; Patent No. US20010016324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gurney, Mark E.

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; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-927-1

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Query Match          100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-795-847-1

; Sequence 1, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES

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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-847-1

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Query Match          100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320

Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

# RESULT 3

US-09-794-743-1

; Sequence 1, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493



Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

Qy 1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGACGCGTCGCCCC 1500  
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 Db 1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGACGCGTCGCCCC 1500

Qy 1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560  
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 Db 1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy 1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCAGGGC 1620  
 |||  
 Db 1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCAGGGC 1620

Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT 1680  
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 Db 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT 1680

Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 |||  
 Db 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAAAA 1800  
 |||  
 Db 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAAAA 1800

Qy 1801 AAAA 1804  
 |||  
 Db 1801 AAAA 1804

#### RESULT 4

US-09-794-748-1

; Sequence 1, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24



; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-794-748-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCGCAACTTCTTGCCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCGCAACTTCTTGCCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720

Db	661	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	 CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560

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Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
          |||||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
Qy      1741 CTCCTACTTCCAAGAAAAATAATTAACCAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
          |||||
Db      1741 CTCCTACTTCCAAGAAAAATAATTAACCAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1800
Qy      1801 AAAA 1804
          ||||
Db      1801 AAAA 1804

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RESULT 5

US-09-794-925-1

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; Sequence 1, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-925-1

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Query Match 100.0%; Score 1804; DB 9; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGCCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGCCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840

Db	781	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	 CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTGGGCATTTCCCCA	1200
Db	1141	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTGGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTGCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	 CGTGACCCTGAGGTGCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680

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Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCCACCCGTCTTCAATCTCTGTTCT 1680
Qy      1681 GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAAAAA 1800
Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

```

# RESULT 6

US-09-681-442-1

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; Sequence 1, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-681-442-1

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Query Match      100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          |||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

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Qy	61	GGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGCCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGCCCTAGCT	600
Qy	601	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960

Db	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021		CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021		CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCA	1200
Db	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCA	1200
Qy	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261		AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCGTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261		AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCGTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321		GTGTCTGAAATTTCCGGGCCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321		GTGTCTGAAATTTCCGGGCCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621		AGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621		AGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681		GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681		GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741		CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800



Db 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAAAAA 1800  
Qy 1801 AAAA 1804  
||||  
Db 1801 AAAA 1804

RESULT 7

US-09-869-414-1  
; Sequence 1, Application US/09869414  
; Publication No. US20030077226A1  
; GENERAL INFORMATION:  
; APPLICANT: Beinkowski et al.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280M  
; CURRENT APPLICATION NUMBER: US/09/869,414  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-869-414-1

Query Match 100.0%; Score 1804; DB 10; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60  
|||||  
Db 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60  
  
Qy 61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
|||||  
Db 61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
  
Qy 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
|||||  
Db 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
  
Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCCAACTTCTTGGCCATG 240  
|||||  
Db 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGGCGCCGCCAACTTCTTGGCCATG 240

Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140

Db	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261		AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261		AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321		GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321		GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681		GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681		GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741		CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741		CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801		AAAA 1804	
Db	1801		AAAA 1804	

RESULT 8

US-09-548-366-1

; Sequence 1, Application US/09548366

; Publication No. US20030104365A1

; GENERAL INFORMATION:



Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAACTCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260

Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

RESULT 9

US-09-978-295A-195

; Sequence 195, Application US/09978295A

; Patent No. US20020156006A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
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Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
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Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
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RESULT 10

US-09-978-697-195

; Sequence 195, Application US/09978697

; Patent No. US20020169284A1

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; APPLICANT: Baker Kevin P.  
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; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Shelton, David L.  
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Query Match 98.9%; Score 1784.4; DB 9; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      94 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

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Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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RESULT 11

US-09-978-192A-195

; Sequence 195, Application US/09978192A

; Patent No. US2002017753A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C9  
 ; CURRENT APPLICATION NUMBER: US/09/978,192A  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/064249  
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; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR APPLICATION NUMBER: 60/085697

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Query Match          98.9%;   Score 1784.4;   DB 9;   Length 1879;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 1785;   Conservative    0;   Mismatches    1;   Indels    0;   Gaps    0;

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Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
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Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
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Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
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; Sequence 195, Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
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; APPLICANT: Tumas, Daniel  
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; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
; CURRENT FILING DATE: 2001-10-24  
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Best Local Similarity 99.9%;  Pred. No. 0;
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Db	454	 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
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Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
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Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
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Db	1174	 TACCTGAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1233
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RESULT 13

US-09-978-189-195

; Sequence 195, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
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Query Match          98.9%; Score 1784.4; DB 10; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG 333

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy      301 CCCCCGAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 CCCCCGAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy      421 AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633
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Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473

Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1879

# RESULT 14

US-09-978-608A-195

; Sequence 195, Application US/09978608A

; Publication No. US20030045462A1

## ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.

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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 195
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-978-608A-195
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Query Match          98.9%; Score 1784.4; DB 10; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGGCTCCTGCGCGCC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGGCTCCTGCGCGCC 153

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy     121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG 333

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy     421 AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGGCTTCGTTGGGGAA 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 AAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGGCTTCGTTGGGGAA 573

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT 633
```

Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1234	ATTAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

Db	1474		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594		CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654		GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1680
Db	1714		AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCT	1773
Qy	1681		GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774		GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741		CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834		CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 15

US-09-978-585A-195

; Sequence 195, Application US/09978585A

; Publication No. US20030049633A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.

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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 195
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-978-585A-195
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Query Match          98.9%; Score 1784.4; DB 10; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy     121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCACGGCTTG 273

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCAACTTCTTGGCCATG 333

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCACATTGCCACTATT 633

Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
```

Db	634	 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAA	780
Db	814	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	 CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1234	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440



Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA	1879

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